



wwPDB X-ray Structure Validation Summary Report ⓘ

May 13, 2020 – 06:53 pm BST

PDB ID : 1TGU
Title : The crystal structure of bovine liver catalase without NADPH
Authors : Sugadev, R.; Balasundaresan, D.; Ponnuswamy, M.N.; Kumaran, D.; Swaminathan, S.; Sekar, K.
Deposited on : 2004-05-31
Resolution : 2.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

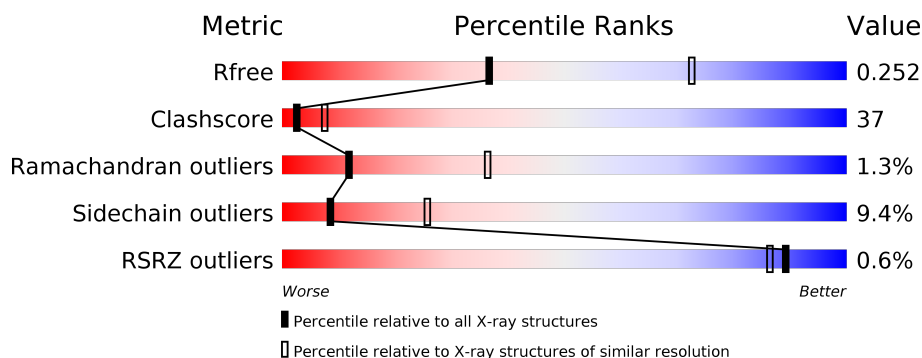
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	506	<div> <div>%</div> <div> <div></div> <div>54%</div> <div>38%</div> <div>6%</div> <div>..</div> </div> </div>
1	B	506	<div> <div>%</div> <div> <div></div> <div>38%</div> <div>51%</div> <div>8%</div> <div>..</div> </div> </div>
1	C	506	<div> <div></div> <div> <div>46%</div> <div>43%</div> <div>8%</div> <div>..</div> </div> </div>
1	D	506	<div> <div>%</div> <div> <div></div> <div>41%</div> <div>53%</div> <div>..</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

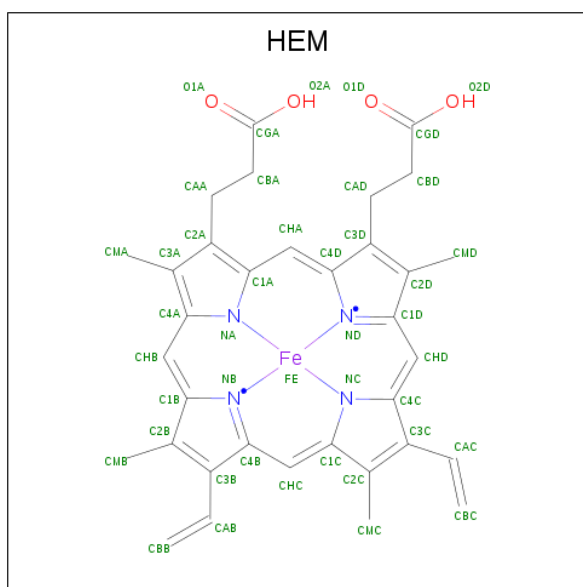
Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	HEM	A	2000	-	-	X	-
2	HEM	B	2001	-	-	X	-
2	HEM	D	2003	-	-	X	-

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Catalase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	499	Total 4017	C 2548	N 715	O 740	S 14	0	0	0
1	B	499	Total 4017	C 2548	N 715	O 740	S 14	0	0	0
1	C	499	Total 4017	C 2548	N 715	O 740	S 14	1	0	0
1	D	499	Total 4017	C 2548	N 715	O 740	S 14	0	0	0

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

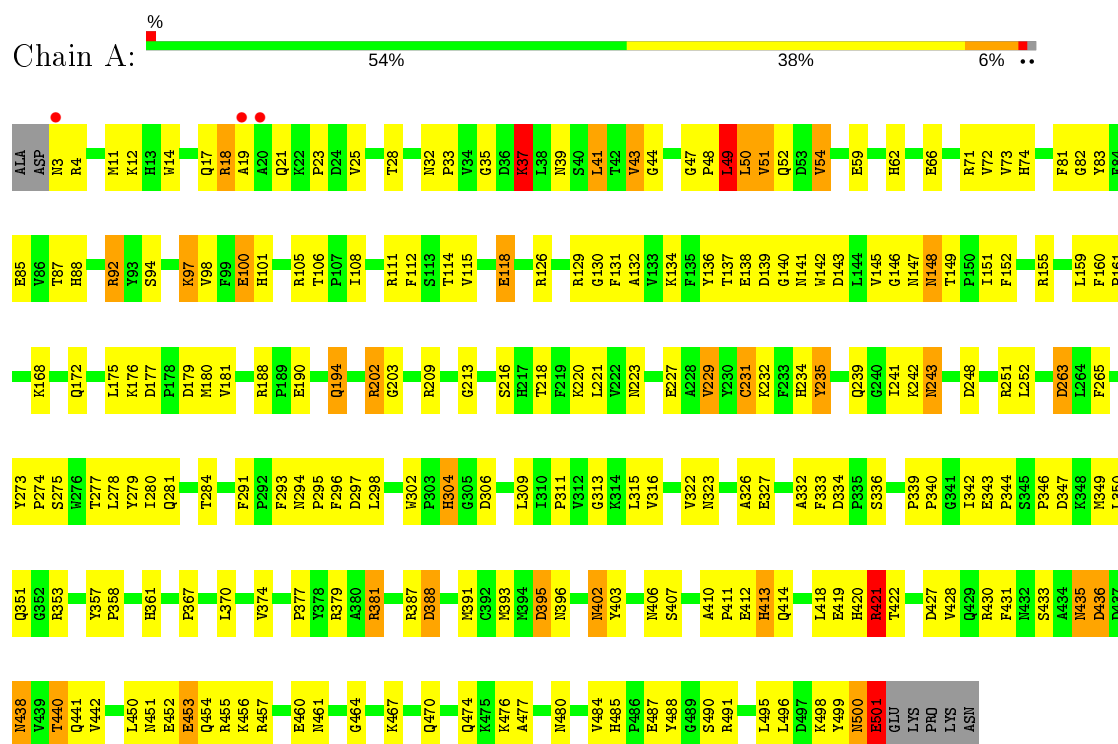
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	229	Total 229	O 229	0	0
3	B	236	Total 236	O 236	0	0
3	C	236	Total 236	O 236	0	0
3	D	232	Total 232	O 232	0	0

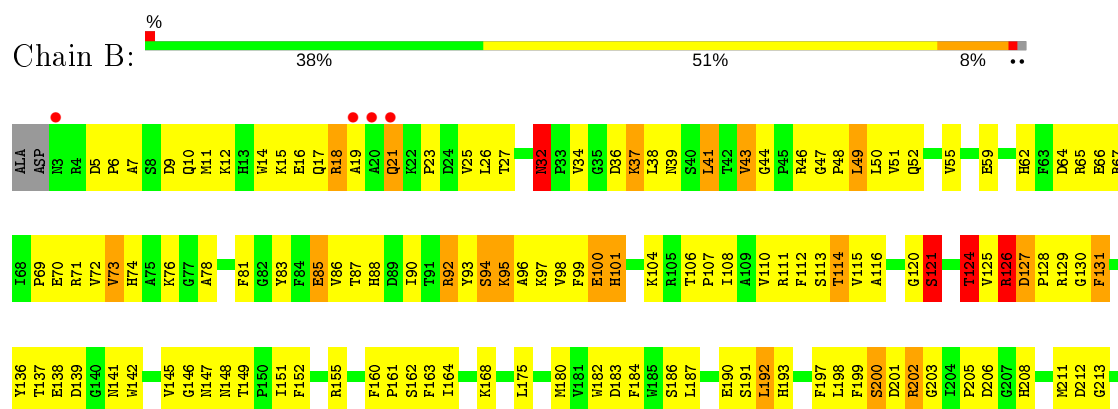
3 Residue-property plots

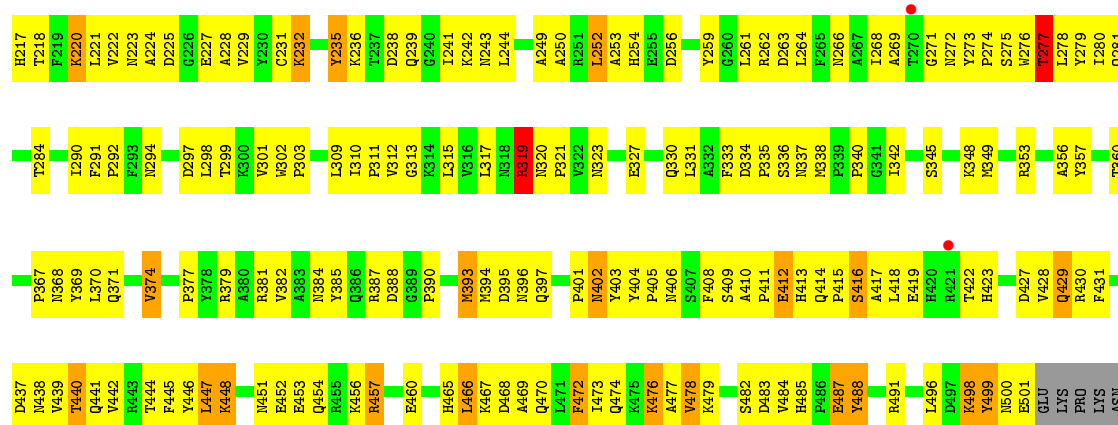
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Catalase



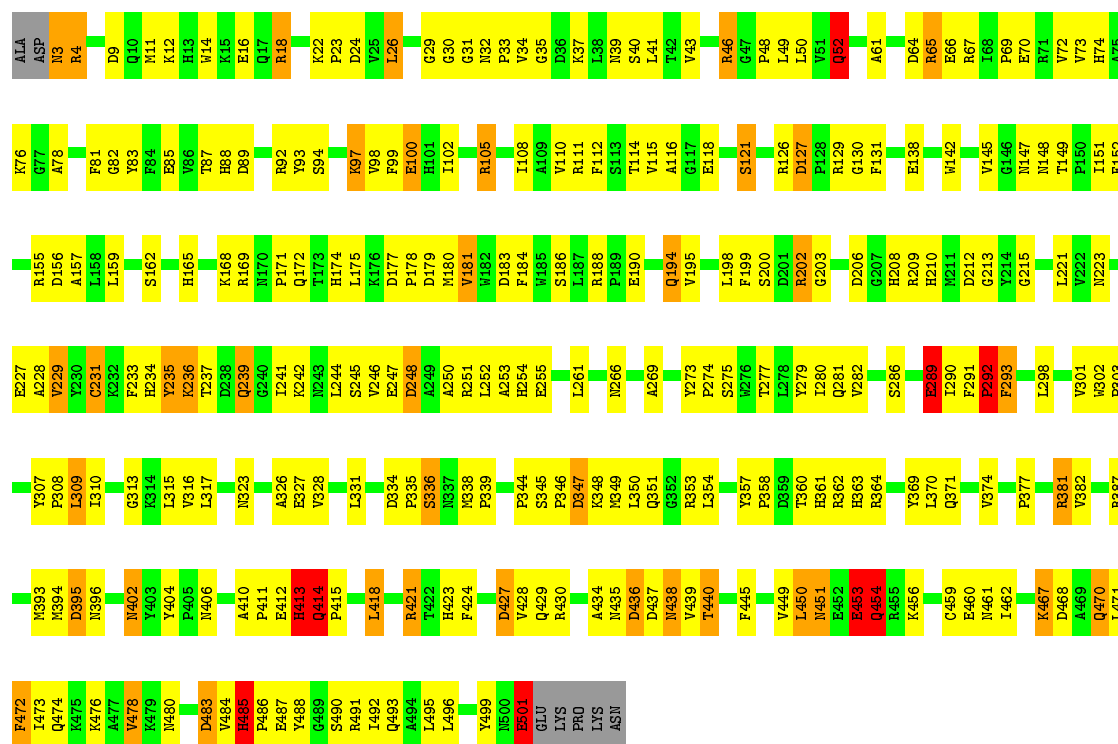
• Molecule 1: Catalase





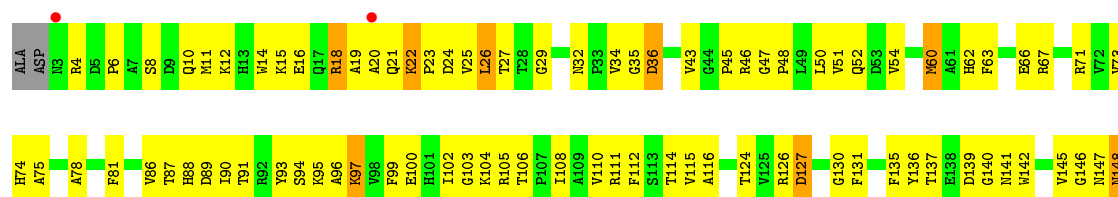
• Molecule 1: Catalase

Chain C: 46% 43% 8% . .



• Molecule 1: Catalase

Chain D: 41% 53% . .



T444	F445	V449	L450	N451	E452	E453	Q454	R455	E460	G464	H465	L466	K467	Q470	K476	A477	V478	K479	N480	V484	H485	P486	E487	Y488	I492	Q493	A494	L495	L496	Y499	M500	GLU	LYS	PRO	LYS	ASN																		
I372	F373	V374	R379	A380	R381	Y385	Q386	R387	D388	G389	P390	M391	C392	M393	M394	D395	N396	Q397	G398	N402	Y403	Y404	F405	M406	S407	F408	S409	A410	P411	E412	H413	Q414	P415	L418	E419	H420	R421	G426	D427	V428	Q429	R430	F431	M432	M435	D436	D437	M438	V439	T440	Q441	V442	R443	
K300	V301	M302	P303	D306	L309	I310	P311	V312	G313	K314	L315	V316	L317	R318	R319	Y324	E327	V328	E329	Q330	L331	A332	F333	D334	N337	M338	P339	I342	S345	P346	D347	R348	M349	L350	Q351	G352	R353	Y357	P358	R359	T360	H361	R362	R363	R364	P367	M368	Y369	L370	Q371				
D225	G226	E227	A228	V229	Y230	C231	K232	F233	H234	Y235	K236	T237	D238	Q239	G240	K242	N243	L244	S245	V246	E247	R251	L261	R262	N266	G271	N272	Y273	P274	S275	W276	T277	L278	Y279	I280	Q281	V282	M283	T284	F285	S286	E287	A288	E289	I290	F291	P292	F293	N294	P295	F296	D297	L298	T299
R155	D156	A157	L158	L159	F160	P161	H165	K168	R169	M170	Q171	T173	D177	P178	D179	M180	W181	W182	D183	S186	L187	R188	P189	E190	S191	L192	H193	Q194	V195	F199	S200	D201	R202	D206	G207	H208	R209	H210	M211	D212	G213	S216	H217	T218	F219	K220	L221	V222	N223	A224				

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	85.53Å 139.67Å 225.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.80 48.76 – 2.79	Depositor EDS
% Data completeness (in resolution range)	89.9 (40.00-2.80) 89.3 (48.76-2.79)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 2.77Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.200 , 0.249 0.201 , 0.252	Depositor DCC
R_{free} test set	1822 reflections (3.00%)	wwPDB-VP
Wilson B-factor (Å ²)	29.9	Xtriage
Anisotropy	0.532	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 51.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	17173	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.85% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HEM

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.56	5/4137 (0.1%)	1.38	52/5619 (0.9%)
1	B	0.97	4/4137 (0.1%)	1.47	28/5619 (0.5%)
1	C	0.66	8/4137 (0.2%)	1.49	33/5619 (0.6%)
1	D	0.60	1/4137 (0.0%)	0.81	6/5619 (0.1%)
All	All	0.72	18/16548 (0.1%)	1.32	119/22476 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	1
1	B	0	2
1	C	2	2
All	All	3	5

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	319	ARG	CD-NE	49.59	2.30	1.46
1	D	413	HIS	CA-CB	-20.44	1.08	1.53
1	C	202	ARG	NE-CZ	16.98	1.55	1.33
1	B	319	ARG	NE-CZ	16.07	1.53	1.33
1	C	414	GLN	CA-CB	-9.86	1.32	1.53

The worst 5 of 119 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	202	ARG	NE-CZ-NH2	-52.90	93.85	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	319	ARG	NE-CZ-NH1	-46.73	96.93	120.30
1	C	202	ARG	NE-CZ-NH1	43.98	142.29	120.30
1	B	319	ARG	CG-CD-NE	-41.22	25.24	111.80
1	B	395	ASP	N-CA-CB	-31.45	53.99	110.60

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	395	ASP	CA
1	C	453	GLU	CA
1	C	501	GLU	CA

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	421	ARG	Sidechain
1	B	126	ARG	Sidechain
1	B	319	ARG	Sidechain
1	C	289	GLU	Sidechain
1	C	292	PRO	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4017	0	3840	292	0
1	B	4017	0	3840	394	0
1	C	4017	0	3839	323	2
1	D	4017	0	3839	315	0
2	A	43	0	30	36	0
2	B	43	0	30	28	0
2	C	43	0	30	18	0
2	D	43	0	30	29	0
3	A	229	0	0	22	0
3	B	236	0	0	28	2
3	C	236	0	0	21	2
3	D	232	0	0	18	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	17173	0	15478	1161	3

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 37.

The worst 5 of 1161 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:421:ARG:HD2	1:B:429:GLN:CG	1.19	1.58
1:B:353:ARG:HG3	2:B:2001:HEM:CBB	1.34	1.57
1:D:147:ASN:ND2	2:D:2003:HEM:CAC	1.74	1.50
1:B:353:ARG:CG	2:B:2001:HEM:HBB2	1.02	1.49
1:D:147:ASN:ND2	2:D:2003:HEM:HAC	1.27	1.44

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:85:GLU:OE2	3:C:2084:HOH:O[3_645]	2.15	0.05
3:B:2109:HOH:O	3:C:2220:HOH:O[3_655]	2.15	0.05
1:C:102:ILE:O	3:B:2221:HOH:O[3_645]	2.16	0.04

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	497/506 (98%)	452 (91%)	42 (8%)	3 (1%)	25	56
1	B	497/506 (98%)	419 (84%)	70 (14%)	8 (2%)	9	31
1	C	497/506 (98%)	434 (87%)	55 (11%)	8 (2%)	9	31
1	D	497/506 (98%)	435 (88%)	55 (11%)	7 (1%)	11	34

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1988/2024 (98%)	1740 (88%)	222 (11%)	26 (1%)	12	36

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	ALA
1	B	100	GLU
1	B	124	THR
1	D	36	ASP
1	A	440	THR

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	431/437 (99%)	396 (92%)	35 (8%)	11	33
1	B	431/437 (99%)	380 (88%)	51 (12%)	5	16
1	C	431/437 (99%)	387 (90%)	44 (10%)	7	22
1	D	431/437 (99%)	399 (93%)	32 (7%)	13	37
All	All	1724/1748 (99%)	1562 (91%)	162 (9%)	8	26

5 of 162 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	402	ASN
1	C	34	VAL
1	D	392	CYS
1	B	416	SER
1	B	488	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 68 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	32	ASN
1	C	414	GLN
1	D	386	GLN
1	C	52	GLN
1	C	239	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	HEM	B	2001	1	27,50,50	2.15	7 (25%)	17,82,82	0.84	1 (5%)
2	HEM	D	2003	1	27,50,50	1.79	6 (22%)	17,82,82	0.84	1 (5%)
2	HEM	C	2002	1	27,50,50	1.80	6 (22%)	17,82,82	0.84	1 (5%)
2	HEM	A	2000	1	27,50,50	2.05	6 (22%)	17,82,82	0.84	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	B	2001	1	-	0/6/54/54	-
2	HEM	D	2003	1	-	0/6/54/54	-
2	HEM	C	2002	1	-	0/6/54/54	-
2	HEM	A	2000	1	-	0/6/54/54	-

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2001	HEM	C4A-CHB	6.22	1.58	1.41
2	A	2000	HEM	CMC-C2C	-5.40	1.38	1.51
2	B	2001	HEM	C3B-CAB	-4.51	1.38	1.47
2	D	2003	HEM	C3B-CAB	-4.49	1.38	1.47
2	C	2002	HEM	C3B-CAB	-4.47	1.38	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2001	HEM	CBA-CAA-C2A	-2.40	108.05	112.49
2	C	2002	HEM	CBA-CAA-C2A	-2.39	108.08	112.49
2	D	2003	HEM	CBA-CAA-C2A	-2.38	108.10	112.49
2	A	2000	HEM	CBA-CAA-C2A	-2.36	108.13	112.49

There are no chirality outliers.

There are no torsion outliers.

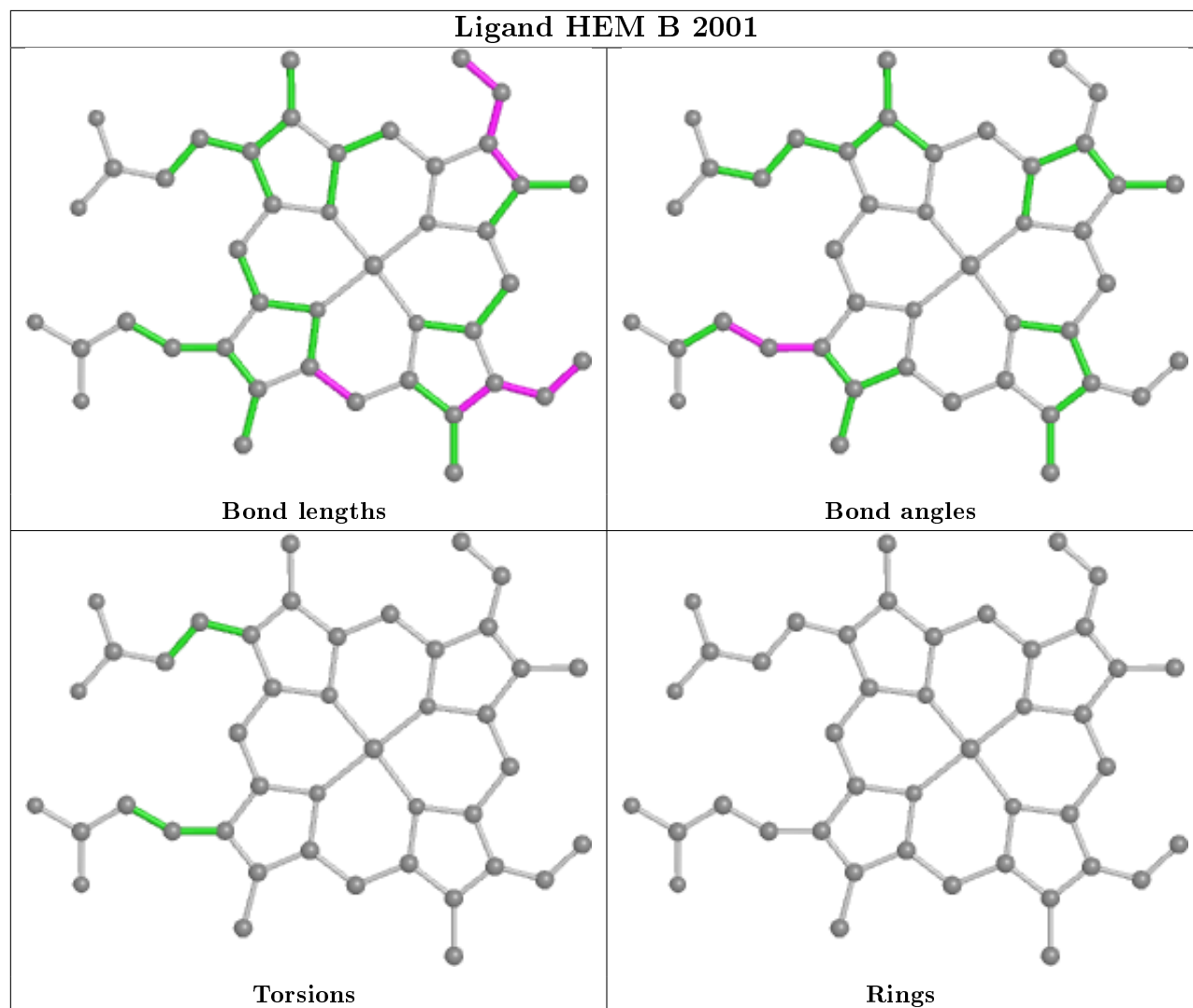
There are no ring outliers.

4 monomers are involved in 111 short contacts:

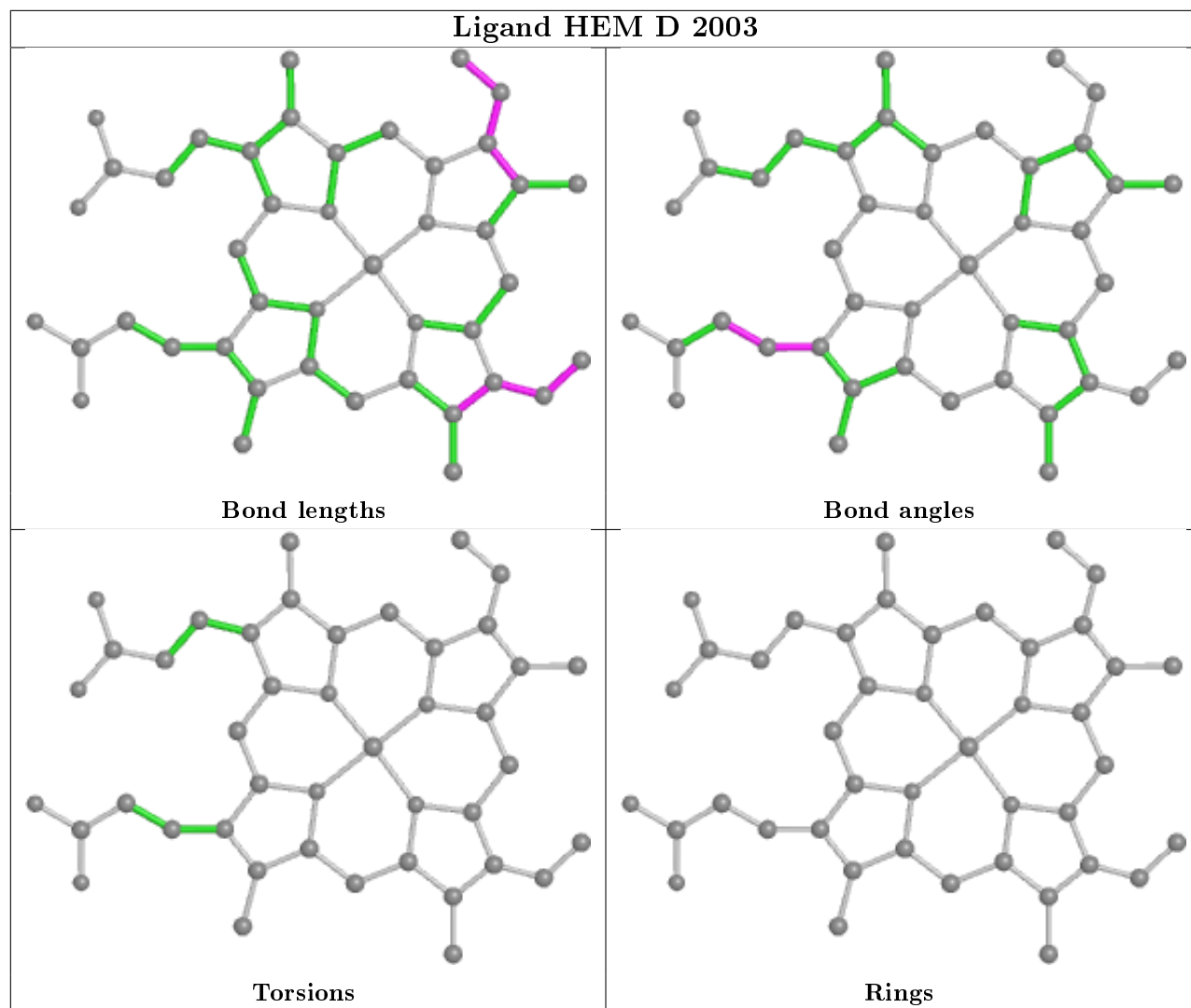
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2001	HEM	28	0
2	D	2003	HEM	29	0
2	C	2002	HEM	18	0
2	A	2000	HEM	36	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

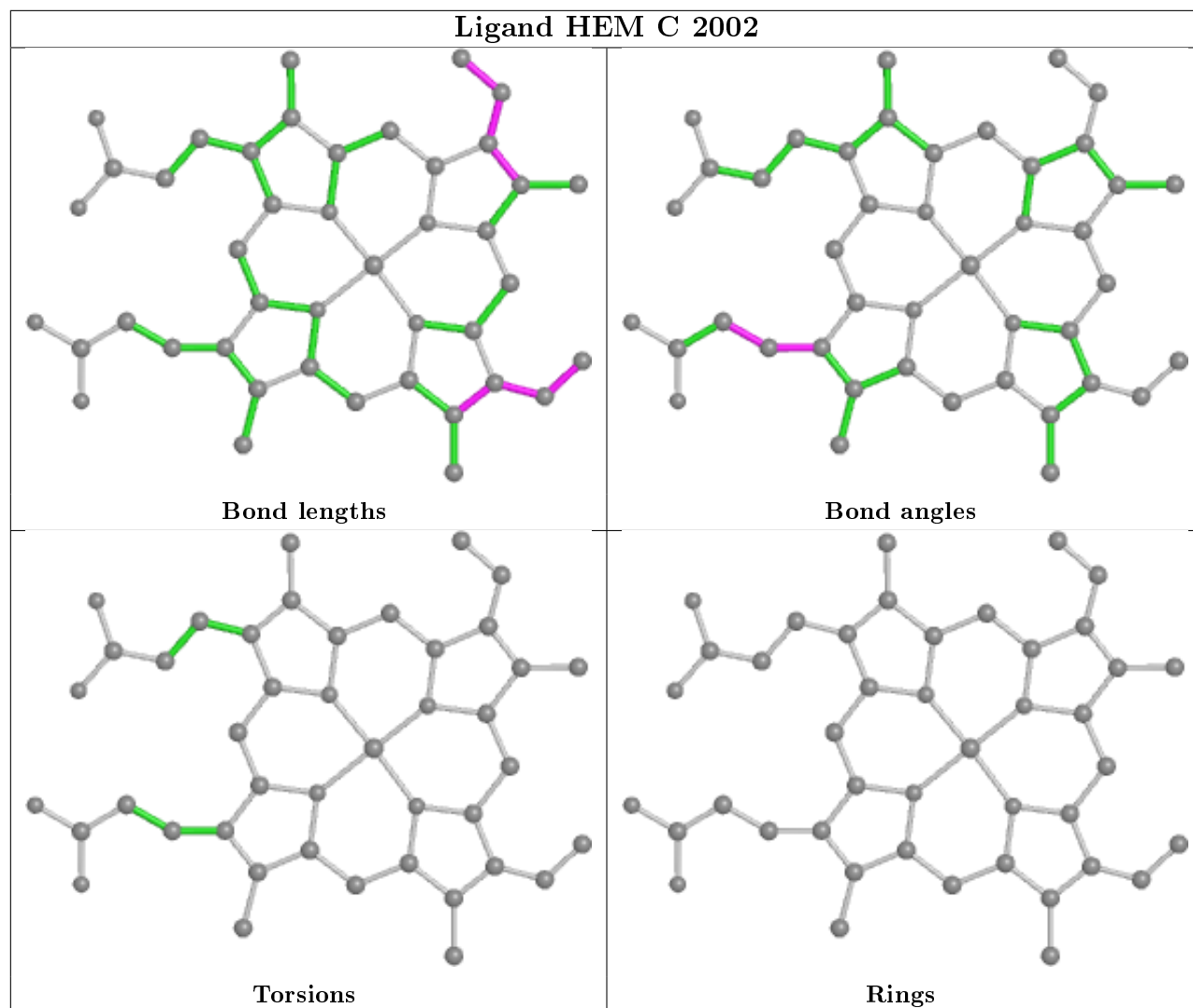
any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

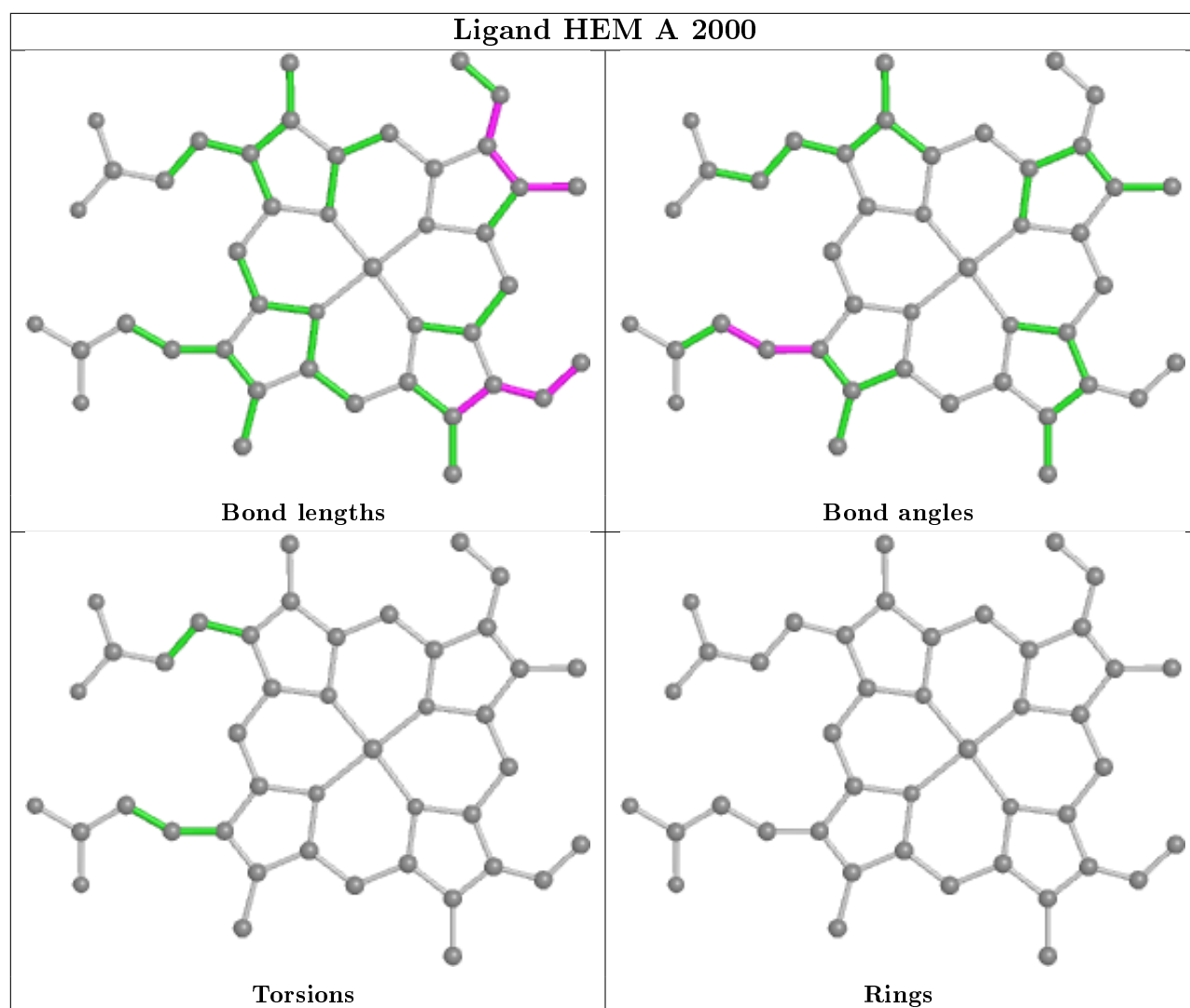


Ligand HEM D 2003



Ligand HEM C 2002





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	499/506 (98%)	-0.49	3 (0%) 89 86	8, 24, 48, 89	0
1	B	499/506 (98%)	-0.33	6 (1%) 79 73	10, 31, 56, 88	0
1	C	499/506 (98%)	-0.44	0 100 100	6, 27, 56, 81	1 (0%)
1	D	499/506 (98%)	-0.35	3 (0%) 89 86	10, 30, 60, 87	0
All	All	1996/2024 (98%)	-0.40	12 (0%) 89 86	6, 28, 55, 89	1 (0%)

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	20	ALA	5.4
1	B	20	ALA	3.9
1	A	3	ASN	3.4
1	B	19	ALA	2.7
1	A	19	ALA	2.6

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

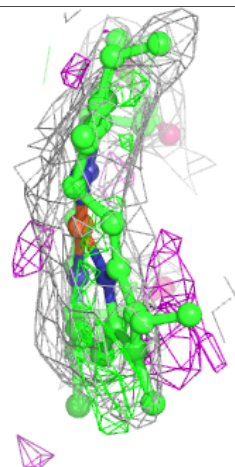
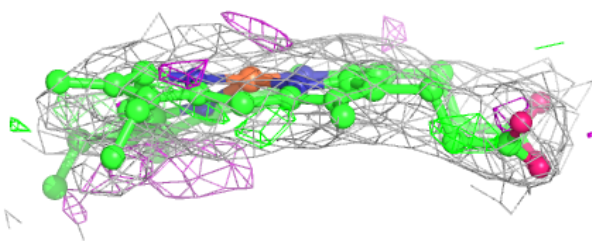
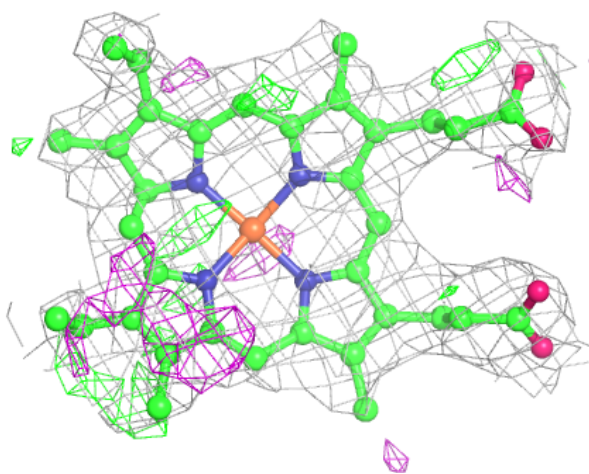
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	HEM	B	2001	43/43	0.92	0.25	16,35,50,71	0
2	HEM	D	2003	43/43	0.93	0.22	17,33,49,60	0
2	HEM	A	2000	43/43	0.95	0.19	4,30,44,49	0
2	HEM	C	2002	43/43	0.96	0.16	15,31,42,91	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

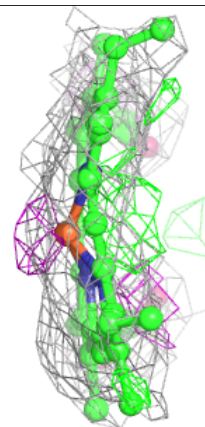
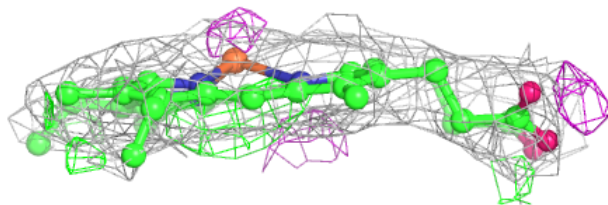
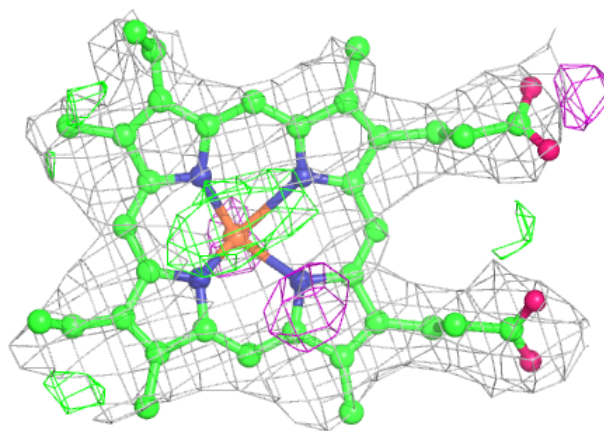
Electron density around HEM B 2001:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



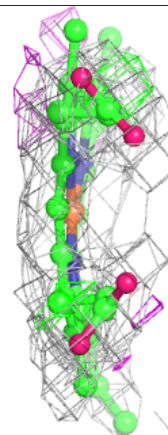
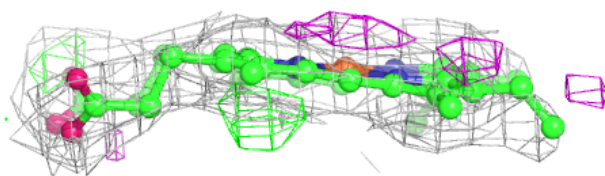
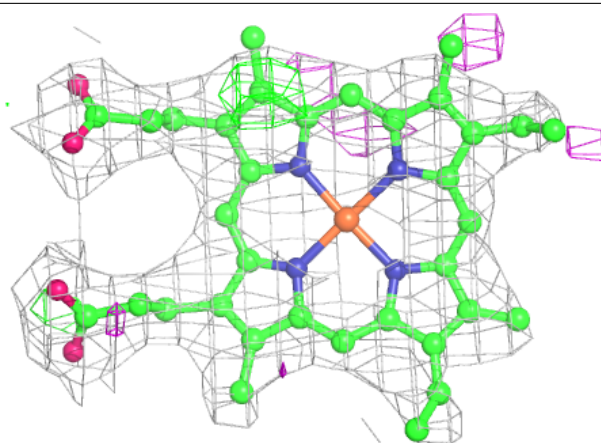
Electron density around HEM D 2003:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



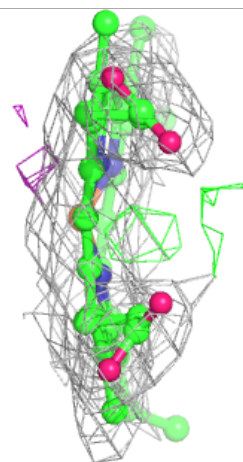
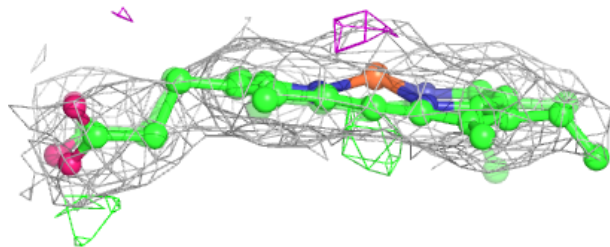
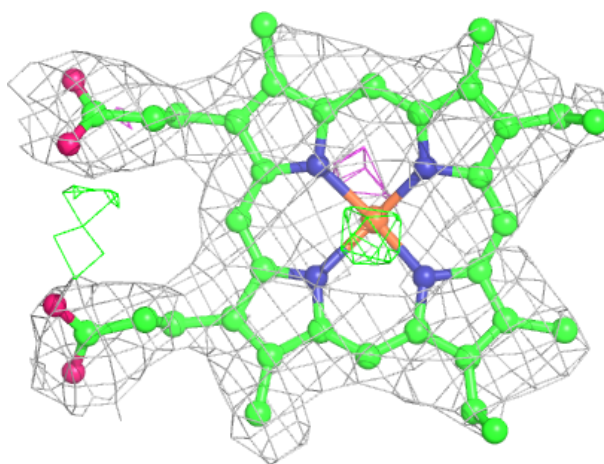
Electron density around HEM A 2000:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM C 2002:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.